

155023

LB

From: Chan, Christina
 Sent: Tuesday, May 31, 2005 5:32 PM
 To: Bausch, Sarae; STIC-Biotech/ChemLib
 Subject: 40332 RE: sequence rush request 10/009340

CRPB

Please rush. Thanks Chris

10-009340

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
 (571)-272-0841
 Remsen, 3E89

-----Original Message-----

From: Bausch, Sarae
 Sent: Tuesday, May 31, 2005 1:01 PM
 To: Chan, Christina
 Subject: sequence rush request 10/009340

Could I get a rush nucleic acid sequence search for SEQ ID No. 1 (932 nt)? Please print out the first 100 hits.

Thank you.

Sarae Bausch, Ph.D.
 USPTO Art Unit 1634
 REM 2 E 84
 Mailbox: REM 2 C 70
 (571) 272-2912

1-932 NA
 LB

STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-
 Date Searcher Picked up: _____
 Date Completed: _____
 Searcher Prep/Rev. Time: _____
 Online Time: _____

 Type of Search
 NA#: _____ AA#: _____
 Interference: _____ SPDI: _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure#: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable.

STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
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 WWW/Internet: _____
 Other(Specify): _____

Date completed: 6-3
 Searcher: Beverly e 2528
 Terminal time: _____
 Elapsed time: _____
 CPU time: _____
 Total time: _____
 Number of Searches: _____
 Number of Databases: _____

Search Site

____ STIC
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 ____ Pre-S

Vendors

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 ____ STN
 ____ Dialog
 ____ APS
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 ____ SDC
 ____ DARC/Questel
 Other CGN

Type of Search

____ N.A. Sequence
 ____ A.A. Sequence
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 ____ Bibliographic

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OM nucleic - nucleic search, using bw model

Run on: June 2, 2005, 16:52:41 ; Search time 203 Seconds

(without alignments)
7512.364 Million cell updates/sec

Title: US-10-009-340-1

Perfect score: 932

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Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:

2405568

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Issued Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

07/07/04

SUMMARIES

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c 2	78.6	8.4	2182	4 US-09-669-380-A-8	Sequence 8, Appli
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c 4	77	8.3	1441	4 US-09-220-132-39	Sequence 39, Appli
c 5	75.6	8.1	960	4 US-09-248-196A-6497	Sequence 6497, Ap
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ALIGNMENTS

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RESULT 1
US-09-202-329-1/c
Sequence 1, Application US/09202329A
GENERAL INFORMATION:
  Patent No.: 6676944
  APPLICANT: Dalton, John P
  APPLICANT: Andrews, Stuart J
  TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin
  FILE REFERENCE: 1181-243
  CURRENT APPLICATION NUMBER: US/09/202,329A
  CURRENT FILING DATE: 1999-02-19
  EARLIER APPLICATION NUMBER: GB 9612214.8
  EARLIER FILING DATE: 1996-06-11
  EARLIER APPLICATION NUMBER: PCT/GB97/01573
  EARLIER FILING DATE: 1997-06-11
  NUMBER OF SEQ ID NOS: 21
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO: 1
  LENGTH: 700
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:02:00 ; Search time 3731 Seconds

(without alignments)

9508.416 Million cell updates/sec

Title: US-10-009-340-1

Perfect Score: 932

Sequence: 1 cagctgttagcatcttgatat.....aggacaacaacctggcacag 932

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

Minimum DB Seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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9: 9b_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Match	Length	DB	ID	Description
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60	101.4	BP633999	10.9	773	BP633999	CK2553458 CK2553458	
C	61	BP633999	10.9	790	BP633999	CK2553458 CK2553458	
62	101.4	BP633999	10.9	923	BP633999	CK2553458 CK2553458	
63	100.8	BP633999	10.8	421	BP633999	BP614006 BP614006	
64	99.8	BP633999	10.7	606	BP633999	CK087314 A002P63.3	
65	99.8	BP633999	10.7	951	BP633999	CK429463 CK429463	
66	99.6	BP633999	10.7	429	BP633999	BP606897 BP606897	
67	99.6	BP633999	10.6	662	BP633999	CN744157 SAL_0507	
C	68	BP633999	10.6	662	BP633999	CN247172 WS01117.B	
69	98.6	BP633999	10.6	400	BP633999	AV816610 AV816610	
70	98.6	BP633999	10.6	401	BP633999	AV801224 AV801224	
71	98.6	BP633999	10.6	408	BP633999	AV805657 AV805657	
C	73	BP633999	10.6	409	BP633999	CK2553458 CK2553458	
C	74	BP633999	10.6	409	BP633999	CK2553458 CK2553458	
C	75	BP633999	10.6	409	BP633999	CK2553458 CK2553458	
C	76	BP633999	10.6	410	BP633999	CK2553458 CK2553458	
C	77	BP633999	10.6	411	BP633999	CK2553458 CK2553458	
C	78	BP633999	10.6	413	BP633999	CK2553458 CK2553458	
C	79	BP633999	10.6	414	BP633999	CK2553458 CK2553458	
C	80	BP633999	10.6	417	BP633999	CK2553458 CK2553458	
C	81	BP633999	10.6	418	BP633999	CK2553458 CK2553458	
C	82	BP633999	10.6	419	BP633999	CK2553458 CK2553458	
C	83	BP633999	10.6	420	BP633999	CK2553458 CK2553458	
C	84	BP633999	10.6	421	BP633999	CK2553458 CK2553458	
C	85	BP633999	10.6	422	BP633999	CK2553458 CK2553458	
C	86	BP633999	10.6	426	BP633999	CK2553458 CK2553458	
C	87	BP633999	10.6	429	BP633999	CK2553458 CK2553458	
C	88	BP633999	10.6	430	BP633999	CK2553458 CK2553458	
C	89	BP633999	10.6	434	BP633999	CK2553458 CK2553458	
C	90	BP633999	10.6	438	BP633999	CK2553458 CK2553458	
C	91	BP633999	10.6	441	BP633999	CK2553458 CK2553458	
C	92	BP633999	10.6	449	BP633999	CK2553458 CK2553458	
C	93	BP633999	10.6	451	BP633999	CK2553458 CK2553458	
C	94	BP633999	10.6	452	BP633999	CK2553458 CK2553458	
C	95	BP633999	10.6	475	BP633999	CK2553458 CK2553458	
C	96	BP633999	10.6	479	BP633999	CK2553458 CK2553458	
C	97	BP633999	10.6	489	BP633999	CK2553458 CK2553458	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 17:59:13 ; Search time 676 Seconds

(without alignments)

8475.441 Million Cell updates/sec

Title: US-10-009-340-1

Perfect score: 932

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters:

11413164

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA : *

1: /cgn2_6_ptodata/2_pubbra/US07_PUBCOMB.seq:*

2: /cgn2_6_ptodata/2_pubbra/PCT_NEW_PUB.seq:*

3: /cgn2_6_ptodata/2_pubbra/US05_NEW_PUB.seq:*

4: /cgn2_6_ptodata/2_pubbra/US06_PUBCOMB.seq:*

5: /cgn2_6_ptodata/2_pubbra/US07_NEW_PUB.seq:*

6: /cgn2_6_ptodata/2_pubbra/US08_PUBCOMB.seq:*

7: /cgn2_6_ptodata/2_pubbra/PCTUS_PUBCOMB.seq:*

8: /cgn2_6_ptodata/2_pubbra/US08_NEW_PUB.seq:*

9: /cgn2_6_ptodata/2_pubbra/US09_PUBCOMB.seq:*

10: /cgn2_6_ptodata/2_pubbra/US09C_PUBCOMB.seq:*

11: /cgn2_6_ptodata/2_pubbra/US10_PUBCOMB.seq:*

12: /cgn2_6_ptodata/2_pubbra/US10F_PUBCOMB.seq:*

13: /cgn2_6_ptodata/2_pubbra/US10_PUBCOMB.seq:*

14: /cgn2_6_ptodata/2_pubbra/US10B_PUBCOMB.seq:*

15: /cgn2_6_ptodata/2_pubbra/US10C_PUBCOMB.seq:*

16: /cgn2_6_ptodata/2_pubbra/US10D_PUBCOMB.seq:*

17: /cgn2_6_ptodata/2_pubbra/US10E_PUBCOMB.seq:*

18: /cgn2_6_ptodata/2_pubbra/US10F_PUBCOMB.seq:*

19: /cgn2_6_ptodata/2_pubbra/US10G_PUBCOMB.seq:*

20: /cgn2_6_ptodata/2_pubbra/US11_PUB.seq:*

21: /cgn2_6_ptodata/2_pubbra/US60_NEW_PUB.seq:*

22: /cgn2_6_ptodata/2_pubbra/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score: 104

Query: 11.2

Match: 1335

Length: 9

DB: US-09-938-842A-622

ID: Sequence 622, APP

Description: Sequence 622, APP

Score: 104

Query: 11.2

Match: 1335

Length: 9

DB: US-09-938-842A-622

ID: Sequence 622, APP

Description: Sequence 622, APP

Score: 100

Query: 10.8

Match: 773

Length: 17

DB: US-10-333-184-431

ID: Sequence 431, APP

Description: Sequence 431, APP

Score: 99

Query: 10.6

Match: 465

Length: 9

DB: US-09-770-444-806

ID: Sequence 806, APP

Description: Sequence 806, APP

Score: 98

Query: 10.6

Match: 586

Length: 17

DB: US-10-333-184-303

ID: Sequence 303, APP

Description: Sequence 303, APP

Score: 98

Query: 10.6

Match: 641

Length: 17

DB: US-09-910-664-68

ID: Sequence 66, APP

Description: Sequence 66, APP

Score: 98

Query: 10.6

Match: 641

Length: 17

DB: US-09-770-445-241

ID: Sequence 241, APP

Description: Sequence 241, APP

Score: 98.2

Query: 10.5

Match: 996

Length: 9

DB: US-10-021-323-12510

ID: Sequence 12510, A

Description: Sequence 12510, A

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c 13	98.2	10.4	1822	18	US-10-425-115-172656
c 14	97	10.4	100	18	US-10-021-323-11357
c 15	93.4	10.0	514	17	US-10-424-599-142308
c 16	93.4	10.0	1954	17	US-10-424-599-142308
c 17	92.6	9.9	1791	17	US-10-424-599-142308
c 18	90.6	9.7	443	18	US-10-021-323-15101
c 19	90.6	9.7	444	18	US-10-021-323-16704
c 20	90.6	9.7	512	18	US-10-021-323-16920
c 21	90.6	9.7	528	18	US-10-021-323-10302
c 22	90.6	9.7	531	18	US-10-021-323-12560
c 23	89.6	9.7	569	18	US-10-021-323-8892
c 24	90.6	9.6	530	18	US-10-021-323-17161
c 25	90.6	9.6	559	18	US-10-021-323-10831
c 26	89.6	9.6	582	18	US-10-021-323-17838
c 27	90.6	9.7	592	18	US-10-021-323-11394
c 28	90.6	9.7	608	18	US-10-021-323-10160
c 29	90.6	9.7	1762	18	US-10-767-795-6451
c 30	89.6	9.6	1791	17	US-10-021-323-17161
c 31	89.6	9.6	1929	17	US-10-424-599-142276
c 32	89.6	9.6	1840	17	US-10-424-599-142286
c 33	89.6	9.6	1704	17	US-10-425-115-175282
c 34	89	9.5	1815	17	US-10-424-599-10860
c 35	89	9.5	1350	9	Sequence 10860, A
c 36	89	9.5	1350	11	Sequence 109-938-842A-1845
c 37	88.6	9.5	621	17	US-10-424-599-134384
c 38	88.6	9.5	1840	17	US-10-424-599-142286
c 39	88.4	9.4	1704	17	Sequence 175282, A
c 40	88.4	9.4	2311	17	Sequence 79417, A
c 41	87.8	9.4	494	18	Sequence 13438, A
c 42	87.8	9.4	588	16	Sequence 13438, A
c 43	87.8	9.4	890	17	Sequence 13438, A
c 44	87.8	9.4	968	18	Sequence 13438, A
c 45	87.8	9.4	1704	17	Sequence 175282, A
c 46	87.8	9.4	1707	17	Sequence 3823, A
c 47	87.8	9.4	1845	18	Sequence 169160, A
c 48	87.8	9.4	1948	18	Sequence 155283, A
c 49	87.8	9.4	2066	18	Sequence 93240, A
c 50	87.8	9.4	2072	18	Sequence 159187, A
c 51	87.8	9.4	2075	18	Sequence 159188, A
c 52	87.8	9.4	2311	17	Sequence 58521, A
c 53	87.4	9.4	761	17	Sequence 169160, A
c 54	87.4	9.4	900	17	Sequence 35442, A
c 55	87.4	9.4	1853	17	Sequence 35442, A
c 56	87.4	9.4	1907	17	Sequence 133716, A
c 57	87.4	9.4	2030	18	Sequence 50161, A
c 58	87.4	9.4	2094	17	Sequence 133718, A
c 59	87	9.3	513	10	Sequence 167, App
c 60	87	9.3	1344	11	Sequence 2342, App
c 61	87	9.3	1936	17	Sequence 2342, App
c 62	87	9.3	623	17	Sequence 4981, App
c 63	86.4	9.3	405	17	Sequence 427, App
c 64	86.2	9.2	1142	17	Sequence 3072, A
c 65	86.2	9.2	1646	17	Sequence 3621, App
c 66	86.2	9.2	1735	18	Sequence 171779, A
c 67	86.2	9.2	426	9	Sequence 231, App
c 68	86	9.2	567	17	Sequence 3053, A
c 69	85.8	9.2	834	17	Sequence 31497, A
c 70	85.8	9.2	1081	18	Sequence 140247, A
c 71	85.8	9.2	1334	17	Sequence 30539, A
c 72	85.8	9.2	1670	18	Sequence 140239, A
c 73	85.8	9.2	1827	18	Sequence 49328, A
c 74	85.8	9.2	1855	18	Sequence 140245, A
c 75	85.8	9.2	1915	18	Sequence 140242, A
c 76	85.8	9.2	2115	18	Sequence 140250, A
c 77	85.8	9.2	540	17	Sequence 3828, App
c 78	74	9.1	852	17	Sequence 429, App
c 79	74	9.1	844	9	Sequence 5066, App
c 80	74	9.1	844	9	Sequence 49328, A
c 81	84.8	9.1	84.8	9	Sequence 140245, A
c 82	84.6	9.1	1930	18	Sequence 41161, A
c 83	84.6	9.1	480	18	Sequence 12013, A
c 84	84.6	9.1	666	17	Sequence 3826, App
c 84	84.6	9.1	3607	17	Sequence 3607, App

APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: Sкрип1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO: 622
LENGTH: 1335
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-622

Query Match 11.2%; *Score* 104; *DB* 11; *Length* 1335;
Best Local Similarity 88.3%; *Pred.* No. 8 *8e-13*; *Indels* 0; *Gaps* 0;
Matches 113; *Conservative* 0; *Mismatches* 15;

Qy 4 CTGTAGCATCTGATATTGCTGATACTCAGGCCACAAAGATCCGTTTACTCTCTGCTT 63
Db 1288 CTGTAGCATCTGATATTGCTGATACTCAGGCCACAAAGATCCGTTTACTCTGCTT 1229

Qy 64 CATTAAACTCCATCTGGCCATTCCTCTCGTACCAATGCAAGAACGTTATCTCA 123
Db 1228 CAGTAGACTCCATCTGGCCATTCCTCTCGTACCAATGCAAGAACGTTATCTCA 1169

RESULT 3
US-09-770-445-8
Sequence 8, Application US/09770445
Patent No. US20020023284A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: Sкрип1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/254, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO: 622
LENGTH: 1335
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-622

Query Match 11.2%; *Score* 104; *DB* 9; *Length* 1335;
Best Local Similarity 88.3%; *Pred.* No. 8 *8e-13*; *Indels* 0; *Gaps* 0;
Matches 113; *Conservative* 0; *Mismatches* 15;

Qy 4 CTGTAGCATCTGATATTGCTGATACTCAGGCCACAAAGATCCGTTTACTCTGCTT 63
Db 1288 CTGTAGCATCTGATATTGCTGATACTCAGGCCACAAAGATCCGTTTACTCTGCTT 1229

Qy 64 CATTAAACTCCATCTGGCCATTCCTCTCGTACCAATGCAAGAACGTTATCTCA 123
Db 1228 CAGTAGACTCCATCTGGCCATTCCTCTCGTACCAATGCAAGAACGTTATCTCA 1169

RESULT 2
US-09-938-842A-622/c
Sequence 622, Application US/0938842A
Publication No. US20040003476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2023US (PARA-0122RV)
CURRENT APPLICATION NUMBER: US 60/1770, 445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178, 472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SEQ ID NO: 8
LENGTH: 1469

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:25:44 ; Search time 614 Seconds

(without alignments)

8995.666 Million cell updates/sec

Title: US-10-009-340-1

Perfect score: 932

Sequence: 1 caggtagatccatgtat.....agagcaacaacctggcacag 932

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

8780412

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04 : *

1: geneseqn1980s:*

2: geneseqn1930s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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c 4	104	11.2	1632	3	Aac47401	Arabidops
c 5	104	11.2	1636	3	AAC37579	Arabidops
c 6	100.8	10.8	772	6	ABK31017	Plant dwa
c 7	99.2	10.6	469	6	Abk0849	Plant dwa
c 8	98.6	10.6	445	6	ABL94041	Arabidops
c 9	98.6	10.6	586	6	ABK30889	Plant dwa
c 10	98.6	10.6	641	6	Abk30652	Plant dwa
c 11	98.6	10.6	641	6	ABL49466	Sequence
c 12	98.6	10.6	996	6	ABN98473	Arabidops
c 13	98.6	10.6	1601	3	AAC40829	Arabidops
c 14	98.6	10.6	1604	3	AAC47026	Arabidops
c 15	98.6	10.6	1643	3	AAC48904	Arabidops
c 16	98.2	10.5	524	13	ACN57729	Cotton gy
c 17	98.2	10.5	544	13	ACN61790	Cotton gy
c 18	98.2	10.5	619	13	ADR56169	Cotton cd
c 19	97	10.4	882	3	AAC48727	Arabidops
c 20	97	10.4	1353	12	ADN73732	Thale cre

c 21	97	10.4	1621	3	AAC46796	Arabidops
c 22	97	10.4	1624	3	AAC47378	Arabidops
c 23	97	10.4	1706	3	AAC35010	Arabidops
c 24	95.4	10.2	1430	3	AAC37105	Arabidops
c 25	95.4	10.1	150	3	AAC46947	Arabidops
c 26	94	10.1	1353	3	AAC49119	Arabidops
c 27	93.8	10.1	1611	3	AAC49774	Arabidops
c 28	93.8	10.1	1643	3	AAC49782	Arabidops
c 29	93.8	10.1	1649	3	AAC49781	Arabidops
c 30	93.8	10.1	1649	3	ACN56306	Arabidops
c 31	93.8	10.0	514	13	ACN56576	Cotton gy
c 32	90.6	9.7	443	13	ACN60320	Cotton gy
c 33	90.6	9.7	444	13	ACN61923	Cotton gy
c 34	90.6	9.7	512	13	ACN62139	Cotton gy
c 35	90.6	9.7	528	13	ACN55521	Cotton cd
c 36	90.6	9.7	531	13	ACN57719	Cotton gy
c 37	90.6	9.7	569	13	ACN52111	Cotton cd
c 38	90.6	9.7	573	13	ACN56050	Cotton an
c 39	90.6	9.7	574	13	ACN56613	Cotton gy
c 40	90.6	9.7	608	13	ACN53764	Cotton an
c 41	90.6	9.7	1762	13	ADR65670	Cotton cd
c 42	89.6	9.6	563	13	ACN62380	Cotton gy
c 43	89.6	9.6	559	13	ACN56668	Cotton an
c 44	89.6	9.6	582	13	ACN63057	Cotton cd
c 45	89.6	9.6	592	13	ACN50798	Cotton an
c 46	89	9.5	1350	6	ABZ14040	Arabidops
c 47	89	9.5	1496	3	AAC48427	Arabidops
c 48	89	9.5	1601	3	AAC34041	Arabidops
c 49	87.8	9.4	414	3	AAC46724	Zea mays
c 50	87.8	9.4	476	3	AAC46728	Zea mays
c 51	87.8	9.4	494	13	ACN58557	Cotton gy
c 52	87.8	9.4	588	10	ADI02554	Human cdn
c 53	87.8	9.4	1707	12	ADJ42223	Plant cdn
c 54	87	9.3	441	3	AAC41663	Arabidops
c 55	87	9.3	513	10	ADE81396	Zea mays
c 56	87	9.3	1344	6	ABZ14537	Arabidops
c 57	87	9.3	1564	3	AAC47973	Bacterial
c 58	86.4	9.3	475	3	AC35886	Zea mays
c 59	86.4	9.3	623	12	ADJ43982	Plant cdn
c 60	86.2	9.2	405	6	ABX3103	Arabidops
c 61	86	9.2	426	8	ABX62116	Arabidops
c 62	86	9.2	2833	13	ADS9274	beta-1 tu
c 63	85.8	9.2	567	13	ADS58869	Bacterial
c 64	85	9.1	1347	2	AT41999	Oncocerc
c 65	84.8	9.1	540	12	ADJ43828	Plant cdn
c 66	84.8	9.1	605	6	ABK31015	Arabidops
c 67	84.8	9.1	1623	6	ABK1598	Cotton cd
c 68	84.6	9.1	480	13	ACN57232	Cotton gy
c 69	84.6	9.1	585	13	ADQ5711	Novel cdn
c 70	84.6	9.1	666	12	ADJ43826	Plant cdn
c 71	84.6	9.1	688	12	ADJ44607	Plant cdn
c 72	84.6	9.1	688	12	ADJ43824	Plant cdn
c 73	84.6	9.1	884	12	ADJ44618	Plant cdn
c 74	84.6	9.1	916	12	ADJ45619	Plant cdn
c 75	83.6	9.0	533	9	ACL18164	DNA clone
c 76	83.4	8.9	1347	2	AAT41988	Dirofilar
c 77	83	8.9	488	9	ACL18168	DNA clone
c 78	83	8.9	540	9	ACL18160	DNA clone
c 79	83	8.9	582	9	ACL18144	DNA clone
c 80	83	8.9	598	13	ACN52958	Cotton an
c 81	83	8.9	601	9	ACL18165	DNA clone
c 82	83	8.9	609	9	ACL18177	DNA clone
c 83	83	8.9	617	9	ACL18179	DNA clone
c 84	83	8.9	620	9	ACL18173	DNA clone
c 85	83	8.9	622	9	ACL18178	DNA clone
c 86	83	8.9	663	9	ACL18182	DNA clone
c 87	83	8.9	668	9	ACL18181	DNA clone
c 88	83	8.9	669	9	ACL18170	DNA clone
c 89	83	8.9	680	9	ACL18174	DNA clone
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c 91	83	8.9	693	9	ACL18163	DNA clone
c 92	83	8.9	693	9	ACL18161	DNA clone
c 93	83	8.9	693	9	ACL18180	DNA clone

94	83	8.9	712	9	ACI18171	ACI18171 DNA clone	Db	
95	83	8.9	720	9	ACI18176	ACI18176 DNA clone	Db	
c	96	8.9	736	12	ADJ42829	Plant cDN	Db	
c	97	8.9	815	12	ADJ42827	Plant cDN	Db	
c	98	82.6	8.9	466	13	ACN62110	Cotton 9Y	Db
c	99	82.6	8.9	585	13	ACN52116	Cotton 9Y	Db
c	100	82.6	8.9	596	13	ACN52103	Cotton an	Db
ALIGNMENTS								
RESULT 1								
X	AAF28949	standard; DNA;	932	BP.	QY	61 CTCATTAACCTCCATTAGCTGACTTAACTCTCAATCTCAAGTT 300	Db	
X	AAF28949;				QY	121 TCACATCGGTGATAACCATATCTTACCTCTTACATTGTGAATGGACCAA 180	Db	
X	02-JUL-2002	(First entry)			QY	121 TCACATCGGTGATAACCATATCTTACCTCTTACATTGTGAATGGACCAA 180	Db	
X	Arabidopsis thaliana	fatty acid hydroxylase gene promoter.			QY	181 CCCATTCTTGAAAGAACTGGTAACCAAACATTGATTAACCTACACTTCTC 240	Db	
X	promoter; gene expression; plant; plant tissue; seed; FAH; frost; fatty acid hydroxylase; stress resistance; pest; pathogen; heat; drought; metabolism; antisense; transgene; ds.				QY	181 CCCATTCTTGAAAGAACTGGTAACCAAACATTGATTAACCTACACTTCTC 240	Db	
X	Arabidopsis thaliana.				QY	241 ATTCTATCTTCGTTGACTTAACTGCTGACTTAACTCTCAAGTT 300	Db	
X	WO2000077223-A1.				QY	241 ATTCTATCTTCGTTGACTTAACTGCTGACTTAACTCTCAAGTT 300	Db	
X	21-DEC-2000.				QY	301 AGACATAAAGACAAAGACTAACTATCTCATCACCAGCGCTGCTCAGTGACTATA 360	Db	
X	08-JUN-2000;	2000WO-FR001574.			QY	301 AGACATAAAGACAAAGACTAACTATCTCATCACCAGCGCTGCTCAGTGACTATA 360	Db	
X	10-JUN-1999;	99FR-00007362.			QY	361 TTATTCGTTGATTAAAGAAACATTCTTACAGTAAAGCAATAAATAAT 420	Db	
X	(INRG) INST NAT RECH AGRONOMIQUE.				QY	361 TTATTCGTTGATTAAAGAAACATTCTTACAGTAAAGCAATAAATAAT 420	Db	
X	Dubreucq B,	Lepiniec L,	Caboche M;		QY	421 TATAATCAAAACATCTGTTGACACTGGTACGTGTTGAGTAATCTACATC 480	Db	
X	WPI: 2001-080694/09.				QY	421 TATAATCAAAACATCTGTTGACACTGGTACGTGTTGAGTAATCTACATC 480	Db	
X	New Plant Promoter from the fatty acid hydroxylase gene, useful for expressing transgenes that e.g. improve stress resistance, in all tissues except ripening and dry seed.				QY	481 ATAGAGGGCGCATCAAATCCTAAATAAGCTATAATTGATTACATAATTCT 540	Db	
X	Claim 3; Page 25; 33pp; French.				QY	481 ATAGAGGGCGCATCAAATCCTAAATAAGCTATAATTGATTACATAATTCT 540	Db	
X	The invention relates to the isolation of a novel promoter that provides expression of a gene in all plant tissues other than ripening and dry seeds at least 80% identical with at least part of the Arabidopsis FAH (fatty acid hydroxylase) gene promoter. The promoter and related promoters from other plants, are used to direct expression of the gene that (i) improve resistance to stress (e.g. pest, pathogens, heat, frost, drought etc.); (ii) to modulate development; (iii) encode enzymes involved in metabolic processes or (iv) inhibit a target gene (by co-suppression or antisense techniques). Transgenes are expressed in all tissues of the adult plant but not its expression product is not present in seeds (so such seeds are likely to be more acceptable to consumers). This sequence represents the promoter region of the FAH gene from A. thaliana				QY	541 ATTTCATCTGTTGAAATTCGAGATTTCTTACATTCTTCTGAACTTTCTGAA 600	Db	
X	Sequence 932 BP; 318 A; 174 C; 141 G; 299 T; 0 U; 0 Other;				QY	541 ATTTCATCTGTTGAAATTCGAGATTTCTTCTGAACTTTCTGAA 600	Db	
X	Query Match 100.0%; Score 932; DB 5; Length 932;				QY	601 TTAAATTCTACTCAGAAAGACCAACTTAACTTCTGAACTTTCTGAA 660	Db	
X	Best Local Similarity 100.0%; Pred. No. 4.5e-191; Mismatches 0; Indels 0; Gaps 0;				QY	601 TTAAATTCTACTCAGAAAGACCAACTTAACTTCTGAACTTTCTGAA 660	Db	
X	Matches 932; Conservative 0; DB 5; Length 932;				QY	661 ATATGTTAAAGCAGTCATAAACTTTGACATGTTGGCAGAAAGCCAATAATTCTGAA 720	Db	
X	Db2817/C				QY	661 ATATGTTAAAGCAGTCATAAACTTTGACATGTTGGCAGAAAGCCAATAATTCTGAA 720	Db	
X	RESULT 2				QY	781 ATAAGTTGAAATTGTAAATATAGTGTAAATGTTTCTTCTCCAT 780	Db	
X	ID ABZ12817	standard; DNA; 1335 BP.			QY	781 ATAAGTTGAAATTGTAAATGTTTCTTCTCCAT 780	Db	
X	XX				QY	841 TGGGATCCTATAAGTGGAGAACAGTGAACAGGCTATGAAAGCTAACTGTATG 900	Db	
X	AC				QY	841 TGGGATCCTATAAGTGGAGAACAGTGAACAGGCTATGAAAGCTAACTGTATG 900	Db	
X	DT 21-JAN-2003 (first entry)				QY	901 AAGAGGCCCCAAAGGCCAACACCTGGCACAG 932	Db	
X	XX				QY	901 AAGAGGCCCCAAAGGCCAACACCTGGCACAG 932	Db	
X	Arabidopsis thaliana	stress regulated gene SEQ ID NO 622.			QY	1 CAGGTGTAGCATCTGTGATTTGGCTGATACCTCAGCCACAGATCGTTCATCTCTC 60	Db	
X	Arabidopsis thaliana	plant; gene; stress; transgenic; ds.			QY	1 CAGGTGTAGCATCTGTGATTTGGCTGATACCTCAGCCACAGATCGTTCATCTCTC 60	Db	
X	KW				QY	61 CTTCATTAAACTCCATCTGTGATTTGGCTGATACCTCAGCCACAGATCGTTCATCTCTC 60	Os	

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:48:24 ; Search time 4373 Seconds

(without alignments)

10327.065 Million cell updates/sec

Title: US-10-009-340-1
 Perfect score: 932

Sequence: 1 caggctgttacatcttgatat.....agagcaacacccggcacag 932

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summariesDatabase : GenBank:
 1: gb_ba:
 2: gb_htg:
 3: gb_in:
 4: gb_om:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_pl:
 9: gb_pr:
 10: gb_ro:
 11: gb_sts:
 12: gb_sy:
 13: gb_un:
 14: gb_vl:
 15: gb_xref:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	932	100.0	932	6 AX058259	AX058259 Sequence
C 2	932	100.0	69817	8 AC003096	AC003096 Arabidopsis
C 3	105.6	11.3	1634	8 BT012803	BT012803 Lycopersici
C 4	104	11.2	1335	6 AX05927	AX05927 Sequence
C 5	104	11.2	1563	8 AT128337	AT128337 Arabidopsis
C 6	104	11.2	1636	8 AY087594	AY087594 Arabidopsis
C 7	104	11.2	2247	8 ATHTUB94	M847056 Arabidopsis
C 8	104	11.2	91570	8 AT113K14	ALU08282 Arabidopsis
C 9	104	11.2	197568	8 ATCHRIV3	ALU161553 Arabidopsis
C 10	100.8	10.8	773	6 AX164424	AX164424 Sequence
C 11	99.2	10.6	469	6 AX364256	AX364256 Sequence
C 12	98.6	10.6	586	6 AX364296	AX364296 Sequence
C 13	98.6	10.6	641	6 AX64059	AX64059 Sequence
C 14	98.6	10.6	641	6 AX366149	AX366149 Sequence
C 15	98.6	10.6	1366	8 AY059075	AY059075 Arabidopsis
C 16	98.6	10.6	1731	8 AY035141	AY035141 Arabidopsis
C 17	98.6	10.6	2336	8 ATHTBT4A	M21415 A.thaliana
C 18	98.6	10.6	60563	8 AB011475	AB011475 Arabidopsis
C 19	97.6	10.5	120562	8 AC124958	AC124958 Medicago

X505928 Eleusine

U91564 Nicotiana

t BT165741 TB82-14 P

BV165739 TB82-5 PC

BV165742 TB82-15 P

X54845 Pea gTUB2 m

AY704406 Quercus p

AP004982 Lotus cor

BT013065 Lyopersici

X54844 P.sativum g

D1544 Xenopus lae

BC049004 Xenopus l

BC074549 Xanthops t

X69467 E.octocarin

X98406 C.arrietum

AJ718573 Nicotiana

BV165740 TB82-6 PC

AX059156 Sequence

D63138 Zinnia eleg

AY081473 Arabidopsis

BT013893 Lycopersici

AY054693 Arabidopsis

M847056 Arabidopsis

AB005244 Arabidopsis

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233382 S.tuberosum

PSGTTUB3

P.sativum g

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